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Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu
55          60          65          70
gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga      338
Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg
          75          80          85
ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag      386
Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys
          90          95          100
aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc      434
Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser
          105          110          115
cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt      482
Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu
          120          125          130
cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga      530
Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg
          135          140          145          150
ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa      578
Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu
          155          160          165
cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca      626
Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro
          170          175          180
acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac      674
Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn
          185          190          195
cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt      725
Gln Ala Glu Ile Ala Ala Cys
          200          205
ggccacactg cccaccaccg acgatgtggg tatggaaccc cctctggata cagaaccctt      785
tcttttccaa ataaaaaaaa aatcatccaa aaaaaaaaaa a      826

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<210> 8

<211> 227

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22..-1

<223> score 8.5

seq AALLLGLMMVVTG/DE

<400> 8

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Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
          -20          -15          -10
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
          -5          1          5          10
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
          15          20          25
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
          30          35          40
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
          45          50          55
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
          60          65          70
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
          75          80          85          90
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
          95          100          105
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
          110          115          120
Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys

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	125		130		135
Val	Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys				
	140		145		150
Met	Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser				
155		160		165	170
Thr	Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala				
	175		180		185
Pro	Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile				
	190		195		200
Ala	Ala Cys				
	205				

<210> 9

<211> 852

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 229..735

<221> sig_peptide

<222> 229..492

<223> score 6.7

seq VFALSSFLNKASA/VY

<400> 9

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tcgtgtcgcc ggcagggagg catagcgctt ctctgatctt cctgcatggc tcaggtgatt	120
ctggacaagg attaagaatg tggatcaagc aggttttttaa atcaagattt aacattccaa	180
cacataaaaa ttatttatcc aacagctcct cccagatcat atactcct atg aaa gga	237
	Met Lys Gly
gga atc tcc aat gta tgg ttt gac aga ttt aaa ata acc aat gac tgc	285
Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr Asn Asp Cys	
-85 -80 -75 -70	
cca gaa cac ctt gaa tca att gat gtc atg tgt caa gtg ctt act gat	333
Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val Leu Thr Asp	
-65 -60 -55	
ttg att gat gaa gaa gta aaa agt ggc atc aag aag aac agg ata tta	381
Leu Ile Asp Glu Glu Val Lys Ser Gly Ile Lys Lys Asn Arg Ile Leu	
-50 -45 -40	
ata gga gga ttc tct atg gga gga tgc atg gca atg cat tta gca tat	429
Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His Leu Ala Tyr	
-35 -30 -25	
aga aat cat caa gat gtg gca gga gta ttt gct ctt tct agt ttt ctg	477
Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser Ser Phe Leu	
-20 -15 -10	
aat aaa gca tct gct gtt tac cag gct ctt cag aag agt aat ggt gta	525
Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser Asn Gly Val	
-5 1 5 10	
ctt cct gaa tta ttt cag tgt cat ggt act gca gat gag tta gtt ctt	573
Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu Leu Val Leu	
15 20 25	
cat tct tgg gca gaa gag aca aac tca atg tta aaa tct cta gga gtg	621
His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser Leu Gly Val	
30 35 40	
acc acg aag ttt cat agt ttt cca aat gtt tac cat gag cta agc aaa	669
Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu Leu Ser Lys	
45 50 55	
act gag tta gac ata ttg aag tta tgg att ctt aca aag ctg cca gga	717
Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys Leu Pro Gly	
60 65 70 75	
gaa atg gaa aaa caa aaa tgaatgaatc aagagtgtt tggttaatgta	765